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OM nucleic - nucleic search, using sw model

Run On: February 16, 2003, 17:00:49 ; Search time 193.217 Seconds
(without alignments)
10829.323 Million cell updates/sec

Title: US-09-497-967-3
Perfect score: 1404
Sequence: 1 atgaataataatttttagt.....tgattttttattattatta 1404

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2773584 seqs, 745158349 residues

Total number of hits satisfying chosen parameters: 5547168

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77.4	5.5	897	6	US-10-144-771-39592
2	65.4	4.7	961	6	US-10-144-771-31796
3	60	4.3	1635	6	US-10-203-138A-8641
4	60	4.3	1973	6	US-10-203-138A-3500
5	53.4	3.8	1188	6	US-10-144-771-4034
6	52.2	3.7	510	6	US-10-203-138A-7146
7	50	3.6	1248	6	US-10-092-411A-1120
8	49	3.5	1141	5	US-09-806-708B-22
9	48	3.4	3532	6	US-10-017-161-1913
10	47.4	3.4	1954	6	US-10-144-771-4707
11	45.8	3.3	1075	6	US-10-203-138A-7632
12	45.8	3.3	1403	6	US-10-203-138A-2529
13	45.8	3.3	3489	6	US-10-194-046-1
14	45.8	3.3	11091	6	US-10-092-411A-2243
15	45	3.2	21423	5	US-09-949-004-601
16	44.4	3.2	583	6	US-10-144-771-29725
17	43.4	3.1	1231	6	US-10-017-161-2047
18	43.2	3.1	38918	6	US-10-017-161-2049
19	43.2	3.1	428573	5	US-09-948-124-119
20	42.8	3.0	439	6	US-10-203-138A-8573
21	42.8	3.0	1664976	5	US-09-692-570-1
22	42.2	3.0	1805	6	US-10-144-771-22890
23	42.2	3.0	7040	6	US-10-311-506-48
24	42.2	3.0	7040	6	US-10-311-507-48
25	42.2	3.0	2323866	5	US-09-948-124-64
26	42	3.0	574	6	US-10-203-138A-227

27	42	3.0	3673778	6	US-10-312-841-1	Sequence 1, Appl
28	41.8	3.0	756	7	US-60-434-832-6082	Sequence 6082, Ap
29	41.6	3.0	729	6	US-10-144-771-31479	Sequence 31479, A
30	41.6	3.0	1118	6	US-10-144-771-33054	Sequence 33054, A
31	41.6	3.0	1141	5	US-09-806-708B-22	Sequence 22, Appl
32	41.2	2.9	203	5	US-09-531-113-35330	Sequence 35330, A
33	41.2	2.9	1083	5	US-09-950-084-2103	Sequence 2103, Ap
34	41.2	2.9	1372	6	US-10-017-161-2245	Sequence 2245, Ap
35	41.2	2.9	3275	6	US-10-144-771-21113	Sequence 21113, A
36	41.2	2.9	5912	6	US-10-311-455-575	Sequence 575, App
37	41.2	2.9	74105	5	US-09-950-084-7446	Sequence 7446, Ap
38	41.2	2.9	580073	4	US-08-545-528D-1	Sequence 1, Appl
39	41	2.9	489	6	US-10-203-138A-5026	Sequence 5026, Ap
40	41	2.9	1278	6	US-10-092-411A-58	Sequence 58, Appl
41	41	2.9	2297	5	US-09-724-676-30403	Sequence 30403, A
42	41	2.9	2297	5	US-09-724-676-30403	Sequence 30403, A
43	41	2.9	2348	5	US-09-724-676-30401	Sequence 30401, A
44	41	2.9	2548	5	US-09-724-676A-30401	Sequence 30401, A
45	41	2.9	2732	5	US-09-724-676-30402	Sequence 30402, A

ALIGNMENTS

RESULT 1

US-10-144-771-39592
; Sequence 39592, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CLO01321
; CURRENT APPLICATION NUMBER: US/10/144.771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 39592
; LENGTH: 897
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-39592
Query Match 5.5%; Score 77.4; DB 6; Length 897;
Best Local Similarity 43.9%; Pred. No. 3.4e-08;
Matches 330; Conservative 0; Mismatches 421; Indels 0; Gaps 0;

QY	222	TCCTGGTGTAAACCAATCCACCTGCTACTGCTAAATTTAGTCACATAATGTAACGTTAA	281
Db	135	TCCTACTGCTACAGCTTCTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	194
QY	282	ATGCGCTGCTGTCGTCGCAATTCGAGTGGAGCAACAGATTATGCCACATAATACACAGA	341
Db	195	TCCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	254
QY	342	ATGCTTTAATGTAGAATTAATTTTATAATGAATAATGCTCCAAATTTTAAATGCAGTGTC	401
Db	255	TCGTACAGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	314
QY	402	TAGTACATGTCACAGCTTGTCCGGTAAACAGATTGGTGGTGCATGCTGCTGCTGCTGCTG	461
Db	315	TCGTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	374
QY	462	CGTACCATTAGTCGCATAATGTAACGTCGATGTCCTACTGCTGCTGCTGCTGCTGCTGCTG	521
Db	375	TCGTACTGCTACTGCTACAGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	434
QY	522	AGTAACTACTGATTTATGTTAGATTCATTCACAGAAATGTTTAAATGTAGACTTAACTTTTA	581
Db	435	TCGTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	494
QY	582	CTATAATGGTAAATGGAATATCTCTTTCAATCAGGTAAAGTTAATGACACACCTTG	641
Db	495	TCGTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	554
QY	642	TCCGGCAATTAACCTGCTAAATGTTGCTTAAAGCTACTTTAGGTAATGATGCTACAATAC	701

[illegible]

Thu Feb 20 11:10:18 2003

Db 139 HHYVTAMNNAWTTMCMDKDDKRTWWKKNNNATGWDDDTKYHMNNNCBVTWVRY 198
Qy 303 TCGAGTGGAGCAACAGATTATGCAGCAATAATCACAGAATGTGTTAAATGTAGAAATAA 362
Db 199 KTDWDSBKRNNGYGBWKKNSYDVTYVWDDCKRKYRVVTRGRNRNVMWABTA 258
Qy 363 TTTTATATGAAATGCTCCAAATTTAATGCGAGTGTAGTACATGCACACCTGTGCC 422
Db 259 HRRYNNNGWTBAMAYRRWTNNNNNAKMKRAKYWGNRBVNST-CTTWKSKTKYV 317
Qy 423 GGTAAACAGAGTGTGTGCTGATTGCTGCTGTTAATGCCGTACCATAGTCGCATAATG 482
Db 318 TSCWANNCRAGDANKDHKKWKSAAAGVYVNNNNNNNNWTKKARHBAWVWHSAAWKW 377
Qy 483 TAAGTGCATGCTCTACTGTGCTACTGCTACTGATGATGAGTAACTACTGATTATGTAG 542
Db 378 HANAHSRKWTBYKRTVMNNNGTMMKRWAWYWKMDMBGTNNNNNGGRTYGG 437
Qy 543 ATCATTACAGAAATGTTAAATGTAGACTTAACTTTTACTATATAATGTAATAATGTA 602
Db 438 WTKKKWWTYYKWKANCKWRADWHTCHNNTTWKMKTYWNNCYWKSMTNGKSHRBA 497
Qy 603 TACTCCTTTCAATCCAGCTAAAGTTAATGCACACCTTGTCCGGCAATTAACACTGTAA 662
Db 498 AVITWVWRRYAHANNNDYWWKACTWYKYBVCSSWNNYAAWYTKSSWNTSYR 557
Qy 663 TGTGCTTAAGTACTTTAGTAAATGATGCTACATAACCCATAATGTAACGTGTGATG 722
Db 558 WKTNSWRSDTRSMGRANNYARABHYKYWNTRWBSHTWBHBRAGAHHYWBMMYB 617
Qy 723 CCTGATGCTACTATAAGTGTGCTGAGTAAATAATTTGGGTAGCACAAAACCTGAATG 782
Db 618 AKCHMKWAKKYAGAGSNNNNNNNNNNNNNNNNNNATCADDYYAASRYVAMANAKWY 677
Qy 783 TACTAATGTGCTCTCACTTTTACAAATAATGCTCTAATTTCAATCCAGTAAATAG 842
Db 678 YKBAANNAYTHANNWGCWNNATDTRTMKNNNNNNNAGTWKNNNNNNNAKNSAAKNY 737
Qy 843 TACATGCTACCTTGGCCAGCAATAAGATTATGCTGCTGAAGCCACTGCAGGTGTGC 902
Db 738 AAAAVKAAKHHWANKWAMRGWHADAABTTDKRNGAYTKYTTNNNNNTYRGVVTNTA 797
Qy 903 CGCTACTTTAGCCAAATAATGCTAATGCTGCCCTGATGCTAGTGCATGCTAGTGG 962
Db 798 ARDGWANN 857
Qy 963 AGCAACTAATGTAATATATAACAGAAATGCTCTAAATG-----TGCTGCTAACT 1015
Db 858 DDRWRBAYTNN 917
Qy 1016 TTTATTTGATGTAATAATTTCTAGCGAGGAAGTAGTAGTGCAGCAATGCTCCAGCAA 1075
Db 918 NNN 977
Qy 1076 ATAAGTTTAAGCGCTGTAGCACTGAGTGGTGTACTGCTTAAATGCTAATGATG 1135
Db 978 CTWYTWMTTTRTYAATRWKTNATGSMTRCNATGKNNNNYTWGKTRWYARMWRM 1037
Qy 1136 CCCTGAATGCCCTGCTGCTACTGCTACTCAGCATGGAACAACATCTACTTATAATAAG 1195
Db 1038 KAMKVMATGSMNTSARWAKYTRAKGWYNNACAWRWKATCYMTDNNWWTACAT'S 1097
Qy 1196 CAGCATCTGAATGTTAAATGTGCTGCCAA 1226
Db 1098 WMATHKYNNHCKNN 1128

RESULT 9
US-10-017-161-1913
; Sequence 1913, Application US/10017161
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI

; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1913
; LENGTH: 3532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(3532)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(437)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2622)..(3332)
; US-10-017-161-1913
Query Match 3.4%; Score 48; DB 6; Length 3532;
Best Local Similarity 44.0%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 204; Conservative 0; Mismatches 260;
Qy 513 TGATGATGCAGTAACACTACTGATTATGTAGATCATTCACAGAATGTGTTAAATGTAGACT 572
Db 2639 TGT 2698
Qy 573 TAACTTTTACTATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 632
Db 2699 TGATGTAATGATGACGGTGATTATAGTATGATGATGATGATGATGATGATGATGATGATG 2758
Qy 633 CACACCTTGTCCGGCAATTAACCTGTAATGTTTAAAGCTACTTTAGGTAATGATGC 692
Db 2759 TGTGCTGATGGTGGTAATGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2818
Qy 693 TACAATAACCGCAATAATGTAACGTTGCATGCGCTGATGCTACTATAAGTCTGCTGGAGT 752
Db 2819 TGATGATGATGGTGTGATCAGCGTGATGATGATGATGATGATGATGATGATGATGATGATG 2878
Qy 753 AATAATATGGTAGCACAACACACTGAATGTACTAATTTGCTCTCTAACTTTTACAATAA 812
Db 2879 TGATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2938
Qy 813 TAATGCTCTCTAAATTTCAATCCAGGTAATAGTACATGCTTACCTTACCTTACCTTACCTT 872
Db 2939 TGACGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2998
Qy 873 TTATGTTGTTGAAGCCACTGCAGGTGGTCCCGCTACTTTAGCCAAATAATGTAATATTGC 932
Db 2999 TGATGTTGATGTTGATAGTATAACGGTGTGATGATGATGATGATGATGATGATGATGATG 3058
Qy 933 ATGCCCTGATGCTACTCAATTTGCTAGTGAGCAACTAATTAATG 976
Db 3059 TGTTGATGGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3102
RESULT 10
US-10-144-771-4707/c
; Sequence 4707, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 4707


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; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 2243
; LENGTH: 11091
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-2243

Query Match      3.3%; Score 45.8; DB 6; Length 11091;
Best Local Similarity 46.9%; Pred. No. 0.63;
Matches 143; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 726 TGATGGTACTATAGTCTGCTCGAGTAAATAATTTGGGTAGCACAAAACACTGAATGTAC 785
Db 3906 TGATGGTATTTGTGAGTGTGGTAGACAAAAGCATAAATGCAATTACACCTGATACATCAAT 3965
QY 786 TAATTGTCCTCACTTTTACAAATAATAATGCTCCTAATTTTCAATCCAGGTAATAGTAC 845
Db 3966 TAAAGAAATGCTTAAATATGATATGATTAAGCAGCTGATAGAAAATAAAATTCATCA 4025
QY 846 ATGCCTACCTTGGCCAGCAAAATAAGATTATGGTGTGAGCCACTGCAGGTGGTCCGCC 905
Db 4026 AAGAATAAATGATGCTACAGATGAAGAAAATTCAGAAGCGAATCGTAAAAATTGAAGAAGC 4085
QY 906 TACTTTAGCCAAATAATGTAATATTCATGCGCCCTGATGCTGCTGCTAATTTTATTTTGA 1025
Db 4086 TAAGATTGAAGCAAAAGATAATTTCAAGCAATAGTACTAGAGATCAAGTAAATGAAGC 4145
QY 966 AACTAATATGTAATATTATAACAGAAATGCTCAATTTGCTGCTAATTTTATTTTGA 1025
Db 4146 GAAACTAATGGAATAATAATAAGAAAATATACACCAGCACTACTGTGAAATCTGA 4205
QY 1026 TGGTA 1030
Db 4206 AGCTA 4210
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RESULT 15
US-09-949-004-601
; Sequence 601, Application US/09949004
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000848
; CURRENT APPLICATION NUMBER: US/09/949,004
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/232,045
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 6961
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 601
; LENGTH: 21423
; TYPE: DNA
; ORGANISM: Human
US-09-949-004-601
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Query Match      3.2%; Score 45; DB 5; Length 21423;
Best Local Similarity 45.4%; Pred. No. 1.1;
Matches 250; Conservative 0; Mismatches 290; Indels 11; Gaps 2;

QY 498 TACTGGTACTGCACCTTGATGATGAGTAACCTACTGATTATGTTAGATCATTCACAGAATG 557
Db 19722 TAATGGTATGCTGCTGATGAGGTGATATGATGAGATGATGATGAGTAAGGTAATGAAAT 19781
QY 558 TGTAAATGTAGACTTAACTTTTACTATAATATGTTAATGTTAATGTTAATGTTAATGTT 617
Db 19782 TCGATGCTGAGGTGATGCTGTAATGTTGATGATGAGGTGATGATGATGATGATGATGATG 19841
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QY 618 AGGTAAAGTTAATGACACACCTTGTTCGGCAATTTAAACCTGCTAATGTTGCTTAAGCTAC 677
Db 19842 CAATGAAGGTGATGATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 19901
QY 678 TTTAGGTAAATGATGCTACATAACCCGATAAATGTAACGTTGCGATGCCCTGATGGTACTAT 737
Db 19902 TGGAACGGAGCATGGTAAAAAGTAGCGGTGATGATTTAAATGATCATGATGATGATGATGAT 19961
QY 738 AAGTGTCTGGAGTAAATAATTTGGGTAGCACAAAACACTGAATGTTACTAATTTGCTCC 797
Db 19962 TGGTGTGTTGATGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 20021
QY 798 TAACTTTTACAATAATAATGCTCCTCAATTTTCA--ATCCAGGTAATAAGTACATGCTACCT 855
Db 20022 TGATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 20081
QY 856 TGCCAGCAAAATAAGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 915
Db 20082 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 20132
QY 916 AATAATGTAATATTGTCATGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
Db 20133 GATGAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 20192
QY 976 GTAAATTTAACAACAAGTCTCTAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1035
Db 20193 GATAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 20252
QY 1036 TTCTAGGCAGG 1046
Db 20253 GATGATGAAGG 20263
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Search completed: February 17, 2003, 01:52:57
Job time : 244.217 secs

